In the Specification

Please replace the paragraph at page 18, lines 7 through 16, with the following paragraph:

The methods of the present invention can be used in humans and non-humans. For example, the methods can be used to assay polymorphisms in animals for veterinary purposes. For instance, they can be used to amplify target sequences known to be associated with susceptibilities to diseases with genetic components, or to detect known genetic defects in purebred animals such as dogs or horses. They can also be used to assess levels of biodiversity in populations of animals, plants, or microorganisms. The invention can be applied in the search for beneficial genetic components in animals and plants, both domesticated and wild, that are used for food, feed, fiber, oils, lumber, or other raw materials. They can be applied in the search for genetic components of strains of pests, parasites or disease organisms that are especially virulent to humans, plants or animals.

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Amendments to the specification are shown in the attached "Marked-Up Version of Amendments" (pages i-iv).

In the Claims

Please cancel Claims 26, 37, 39 and 41.

Claims 1, 6, 8, 14, 19, 28, 33, 42, 44 and 46-49 have been amended and are shown below in amended form. Amendments to the claims are shown in the attached "Marked-Up Version of Amendments" (pages i-iv).

Sub C1 a2

1. (Amended) A method for identifying a collection of polymorphisms from nucleic acid molecules in a sample by analyzing a subset of the molecules, consisting essentially of the steps of:

a. obtaining a nucleic acid-containing sample;

b. treating the nucleic acid molecules in said sample to produce a reduced representation of nucleic acid fragments selected in a sequence-dependent manner by a method comprising:

i. fractionating said nucleic acid molecules to produce nucleic acid fragments; and

ii. selecting a subset of said nucleic acid fragments,

wherein either (i) or (ii) or both (i) and (ii) are performed in a sequence-dependent manner;

a2 contd.

c. analyzing the reduced representation to identify pairs of fragments from the same chromosomal location, wherein fragments from the same chromosomal location are orthologous sequences; and

d. comparing pairs of orthologous sequences to identify polymorphisms between said sequences,

thereby identifying a collection of polymorphisms.

a3 6. (Amended) The method of Claim 3, wherein the individuals share a trait.

a4 8. (Amended) The method of Claim 1, wherein step (b)(i) is performed using one or more restriction endonucleases.

Sub C3 a5 14. (Amended) A method for identifying a collection of polymorphisms from nucleic acid molecules in a sample by analyzing a subset of the molecules, consisting essentially of the steps of:

a. obtaining a nucleic acid-containing sample to be assessed;

b. treating nucleic acid molecules in said sample to produce a reduced representation of nucleic acid fragments selected in a sequence-dependent manner by a method comprising:

i. fractionating said nucleic acid molecules with one or more restriction endonucleases to produce nucleic acid fragments; and

ii. selecting a subset of said nucleic acid fragments using size fractionation;

wherein either (i) or (ii) or both (i) and (ii) are performed in a sequence-dependent manner;

c. analyzing the reduced representation to identify pairs of fragments from the same chromosomal location, wherein fragments from the same chromosomal location are orthologous sequences; and

a5 cont'd.

d. comparing pairs of orthologous sequences to identify polymorphisms between said orthologous sequences,

thereby identifying a collection of polymorphisms from said nucleic acid molecules.

a6 19. (Amended) The method of Claim 16, wherein the individuals share a trait.

28. (Amended) A method for genotyping a nucleic acid sample to determine the nucleotide present at one or more polymorphic sites of nucleic acid fragments contained in a reduced representation, consisting essentially of the steps of:

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a. obtaining a nucleic acid-containing sample;

b. treating the nucleic acid molecules in said sample to produce a reduced representation of nucleic acid fragments selected in a sequence-dependent manner by a method comprising:

Sub C5

i. fractionating said nucleic acid molecules to produce nucleic acid fragments; and

ii. selecting a subset of said nucleic acid fragments,

wherein either (i) or (ii) or both (i) and (ii) are performed in a sequence-dependent manner; and

c. analyzing the nucleic acid fragments contained in the reduced representation to assess the genotype at one or more polymorphic sites,

thereby genotyping a nucleic acid sample to determine the nucleotide present at one or more polymorphic sites of nucleic acid fragments contained in the reduced representation.

a8 33. (Amended) The method of Claim 28, wherein step (c) is performed by attaching oligonucleotide linker sequences to the fragments in the reduced representation and then amplifying said fragments.

a9 42. (Amended) The method of Claim 1, wherein step (c) is performed by the following steps:

a. comparing the sequences of two fragments from the reduced representation, wherein the two sequences are further analyzed if the two sequences are at least 80% identical over at least 80% of the length of the shorter of the two sequences;

b. aligning the two sequences identified from (a), wherein the two sequences are further analyzed if the two sequences are identical over 10 or more contiguous bases within each of the first 50 bases and the last 50 bases of the sequences;

a9 cont'd.

c. identifying candidate single nucleotide polymorphisms in the sequences of (b), wherein the two sequences are further analyzed if the number of candidate single nucleotide polymorphisms does not exceed 1% of the total number of bases in the shorter of the two sequences, wherein two sequences which meet the criteria of (a) - (c) qualify as a candidate match;

d. repeating (a) - (c) for all proposed pairs; and

e. determining the number of candidate matches for the same chromosomal location, wherein said candidate matches are accepted if said number of matches does not exceed expectations,

wherein accepted candidate matches are considered a pair.

44. (Amended) The method of Claim 14, wherein step (c) is performed by the following steps:

Sub C8 a10

a. comparing the sequences of two fragments from the reduced representation, wherein the two sequences are further analyzed if the two sequences are at least 80% identical over at least 80% of the length of the shorter of the two sequences;

b. aligning the two sequences identified from (a), wherein the two sequences are further analyzed if the two sequences are identical over 10 or more contiguous bases within each of the first 50 bases and the last 50 bases of the sequences;

c. identifying candidate single nucleotide polymorphisms in the sequences of (b), wherein the two sequences are further analyzed if the number of candidate single nucleotide polymorphisms does not exceed 1% of the total number of bases in the shorter of the two sequences, wherein two sequences which meet the criteria of (a) - (c) qualify as a candidate match;

d. repeating (a) - (c) for all proposed pairs; and

e. determining the number of candidate matches for the same chromosomal location, wherein said candidate matches are accepted if said number of matches does not exceed expectations,

wherein accepted candidate matches are considered a pair.

46. (Amended) A method for determining a population of polymorphisms from nucleic acid molecules in a sample, consisting essentially of the steps of:

a. obtaining a nucleic acid-containing sample to be assessed;

b. treating nucleic acid molecules in said sample to produce nucleic acid fragments selected in a sequence-dependent manner by a method comprising:

i. fractionating said nucleic acid molecules to produce nucleic acid fragments; and

ii. selecting a subset of said nucleic acid fragments;

wherein either (i) or (ii) or both (i) and (ii) are done in a sequence-dependent manner;

c. selecting from said subset nucleic acid fragments which occur at the same chromosomal locus, thereby producing a pair, and

d. identifying polymorphisms between fragments of a pair;

thereby determining a population of polymorphisms from said nucleic acid-containing sample.

47. (Amended) A method for determining a population of polymorphisms from nucleic acid molecules in a sample, consisting essentially of the steps of:

a. obtaining a nucleic acid-containing sample to be assessed;

b. treating nucleic acid molecules in said sample to produce nucleic acid fragments selected in a sequence-dependent manner by a method comprising:

i. fractionating said nucleic acid molecules with one or more restriction endonucleases to produce nucleic acid fragments; and

ii. selecting a subset of said nucleic acid fragments using size fractionation;

wherein either (i) or (ii) or both (i) and (ii) are done in a sequence-dependent manner;

c. isolating from said subset nucleic acid fragments which occur at the same chromosomal locus, thereby producing a pair, and

d. identifying polymorphisms between fragments of a pair;

thereby determining a population of polymorphisms from said nucleic acid-containing sample.

48. (Amended) A method for genotyping a nucleic acid-containing sample from an individual to determine the nucleotide present at one or more polymorphic sites, the method consisting essentially of:

a. obtaining a first nucleic acid-containing sample to be assessed;

b. treating nucleic acid molecules in said sample to produce a reduced representation of nucleic acid fragments selected in a sequence-dependent manner by a method comprising:

i. fractionating said nucleic acid molecules to produce nucleic acid fragments; and

ii. selecting a subset of said nucleic acid fragments;

wherein either (i) or (ii) or both (i) and (ii) are done in a sequence-dependent manner;

c. analyzing the reduced representation to identify pairs of fragments from the same chromosomal location, wherein fragments from the same chromosomal location are orthologous sequences;

d. comparing pairs of orthologous sequences to identify polymorphisms between the orthologous sequences;

e. obtaining a second nucleic acid-containing sample from an individual to be assessed; and

f. analyzing said second nucleic acid-containing sample to assess the genotype at one or more polymorphisms identified in (d).

thereby genotyping a nucleic acid-containing sample from an individual to determine the nucleotide present at one or more polymorphic sites.

49. (Amended) A method according to Claim 48, wherein the second nucleic acid-containing sample is a sample which has been treated by a method comprising:

i. fractionating the nucleic acid molecules in said sample to produce nucleic acid fragments; and

ii. selecting a subset of said nucleic acid fragments;

wherein either (i) or (ii) or both (i) and (ii) are done in a sequence-dependent manner.